Proteomic Analysis of Human Serum

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Changes in serum proteins that signal histopathological states, such as cancer and other diseases, are useful diagnostic and prognostic biomarkers. Unfortunately the large dynamic concentration range of proteins in serum makes it a challenging proteome to effectively characterize. Most proteomic investigations deplete highly abundant proteins, such as albumin, to decrease this dynamic concentration range. Protein depletion, however, may result in removal of an archive of histopathologically important low abundance proteins that may be bound to the proteins targeted for depletion. In this study, we applied a multidimensional peptide separation strategy combined with tandem mass spectrometry for the identification of proteins in human serum without the need to deplete highly abundant proteins. Our investigation resulted in the identification of over 1500 proteins in serum. We have used gene ontology to classify the proteins identified and find that proteins from all functional classes and cellular locales are present, demonstrating the potential archive of pathophysiological information in serum.

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